



SEQUENCE LISTING

<110> URQUIMA, S.A.

<120> Promotor and constructions for expression of
recombinant proteins in filamentous fungi

<130> Thaumatin 2

<140> PCT/EP 99/02243

<141> 1999-04-01

<150> ES 9800699

<151> 1998-04-02

<160> 13

<170> PatentIn Ver. 2.1

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<212> DNA

<213> Aspergillus awamorii

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<221> intron

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aatcaatcct ccccttcaga atg tct aac ctt cct cac gag ccc gag ttc gag 773
Met Ser Asn Leu Pro His Glu Pro Glu Phe Glu
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cag gcc tac aag ggtatgttcc attgccccctc cgaaattgat gatggaaaaa 825
Gln Ala Tyr Lys
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aaattctaac aacatcctct taca gag ctt gcc tcg acc ctt gag aac tcc 876
Glu Leu Ala Ser Thr Leu Glu Asn Ser
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acc ctc ttc cag aag aac ccc gaa tac cgc aag gcc ctt gct gtc gtc 924
Thr Leu Phe Gln Lys Asn Pro Glu Tyr Arg Lys Ala Leu Ala Val Val
25 30 35 40

tcc gtc ccc gag cgt gtc atc cag ttc cgt gtc gtc tgg gag gat gat 972
Ser Val Pro Glu Arg Val Ile Gln Phe Arg Val Val Trp Glu Asp Asp
45 50 55

gcc ggc aac gtc cag gtc aac cgc ggt ttc cgt gtc cag ttc aac agc 1020
Ala Gly Asn Val Gln Val Asn Arg Gly Phe Arg Val Gln Phe Asn Ser
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gcc ctc ggt ccc tac aag ggt ggt ctt cgt ttc cac ccc tcc gtc aac 1068
Ala Leu Gly Pro Tyr Lys Gly Gly Leu Arg Phe His Pro Ser Val Asn
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ttg tcc atc ctc aag ttc ctt ggt ttc gag cag atc ttc aag aat gct 1116
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Leu Thr Gly Leu Asn Met Gly Gly Gly Lys Gly Gly Ser Asp Phe Asp
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ccc aag ggc aag tcc gac aac gag atc cgt cgc ttc tgt gtt tcc ttc 1212
Pro Lys Gly Lys Ser Asp Asn Glu Ile Arg Arg Phe Cys Val Ser Phe
125 130 135

atg acc gag ctc tgc aag cac atc ggt gcc gac act gat gtt ccc gct 1260
Met Thr Glu Leu Cys Lys His Ile Gly Ala Asp Thr Asp Val Pro Ala
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Gly Asp Ile Gly Val Thr Gly Arg Glu Val Gly Phe Leu Phe Gly Gln
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Tyr Arg Lys Ile Arg Asn Gln Trp Glu Gly Val Leu Thr Gly Lys Gly
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Val Val Tyr	
gcgactaacg cgtaacag tac gtc gag cac atg att gct cac gcc acc aac	1504
Tyr Val Glu His Met Ile Ala His Ala Thr Asn	
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Asn Val Ala Gln Tyr Ala Ala Leu Lys Val Ile Glu Leu Gly Gly Ser	
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Val Val Ser Leu Ser Asp Thr Gln Gly Ser Leu Ile Ile Asn Gly Glu	
250 255 260	
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Gly Ser Phe Thr Pro Glu Glu Ile Glu Leu Ile Ala Gln Thr Lys Val	
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Glu Arg Asn Glu Leu Ala Ser Ile Val Gly Ala Ala Pro Phe Ser Asp	
280 285 290	
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Ala Asn Lys Phe Lys Tyr Ile Ala Gly Ala Arg Pro Trp Val His Val	
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Gly Lys Val Asp Val Ala Leu Pro Ser Ala Thr Gln Asn Glu Val Ser	
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Gly Glu Glu Ala Gln Val Leu Ile Asn Ala Gly Cys Lys Phe Ile Ala	
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Glu Gly Ser Asn Met Gly Cys Thr Gln Glu Ala Ile Asp Thr Phe Glu	
345 350 355	
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Ala His Arg Thr Ala Asn Ala Gly Ala Ala Ala Ile Trp Tyr Ala Pro	
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Gly Lys Ala Ala Asn Ala Gly Gly Val Ala Val Ser Gly Leu Glu Met	
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Ala Gln Asn Ser Ala Arg Leu Ser Trp Thr Ser Glu Glu Val Asp Ala	
395 400 405	

cgt ctt aag gac atc atg cgc gac tgc ttc aag aac ggt ctt gag act 2128
 Arg Leu Lys Asp Ile Met Arg Asp Cys Phe Lys Asn Gly Leu Glu Thr
 410 415 420

gct cag gag tac gcc acc ccc gct gag ggt gtc ctg cct tcc ctg gtg 2176
 Ala Gln Glu Tyr Ala Thr Pro Ala Glu Gly Val Leu Pro Ser Leu Val
 425 430 435

acc gga tcc aac att gcc ggt ttc acc aag gtg gct gcc gcc atg aag 2224
 Thr Gly Ser Asn Ile Ala Gly Phe Thr Lys Val Ala Ala Ala Met Lys
 440 445 450

gac cag ggt gac tgg tgg taaatgcgga aagccgcaaa cccccgcggc 2272
 Asp Gln Gly Asp Trp Trp
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ttatgtcatg acgattatgt agtttgatgt tccctttcag cgcggatgga tagaggcgcc 2332

ggtgttttct tgctagttaa gatggatgca taatgatatc cttttcttaa tctcaaatt 2392

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Tyr Arg Lys Ala Leu Ala Val Val Ser Val Pro Glu Arg Val Ile Gln
 35 40 45

Phe Arg Val Val Trp Glu Asp Asp Ala Gly Asn Val Gln Val Asn Arg
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Gly Phe Arg Val Gln Phe Asn Ser Ala Leu Gly Pro Tyr Lys Gly Gly
 65 70 75 80

Leu Arg Phe His Pro Ser Val Asn Leu Ser Ile Leu Lys Phe Leu Gly
 85 90 95

Phe Glu Gln Ile Phe Lys Asn Ala Leu Thr Gly Leu Asn Met Gly Gly
 100 105 110

Gly Lys Gly Gly Ser Asp Phe Asp Pro Lys Gly Lys Ser Asp Asn Glu
 115 120 125

Ile Arg Arg Phe Cys Val Ser Phe Met Thr Glu Leu Cys Lys His Ile
 130 135 140

Gly Ala Asp Thr Asp Val Pro Ala Gly Asp Ile Gly Val Thr Gly Arg
 145 150 155 160
 Glu Val Gly Phe Leu Phe Gly Gln Tyr Arg Lys Ile Arg Asn Gln Trp
 165 170 175
 Glu Gly Val Leu Thr Gly Lys Gly Gly Ser Trp Gly Gly Ser Leu Ile
 180 185 190
 Arg Pro Glu Ala Thr Gly Tyr Gly Val Val Tyr Tyr Val Glu His Met
 195 200 205
 Ile Ala His Ala Thr Asn Gly Gln Glu Ser Phe Lys Gly Lys Arg Val
 210 215 220
 Ala Ile Ser Gly Ser Gly Asn Val Ala Gln Tyr Ala Ala Leu Lys Val
 225 230 235 240
 Ile Glu Leu Gly Gly Ser Val Val Ser Leu Ser Asp Thr Gln Gly Ser
 245 250 255
 Leu Ile Ile Asn Gly Glu Gly Ser Phe Thr Pro Glu Glu Ile Glu Leu
 260 265 270
 Ile Ala Gln Thr Lys Val Glu Arg Asn Glu Leu Ala Ser Ile Val Gly
 275 280 285
 Ala Ala Pro Phe Ser Asp Ala Asn Lys Phe Lys Tyr Ile Ala Gly Ala
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 Arg Pro Trp Val His Val Gly Lys Val Asp Val Ala Leu Pro Ser Ala
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 Thr Gln Asn Glu Val Ser Gly Glu Glu Ala Gln Val Leu Ile Asn Ala
 325 330 335
 Gly Cys Lys Phe Ile Ala Glu Gly Ser Asn Met Gly Cys Thr Gln Glu
 340 345 350
 Ala Ile Asp Thr Phe Glu Ala His Arg Thr Ala Asn Ala Gly Ala Ala
 355 360 365
 Ala Ile Trp Tyr Ala Pro Gly Lys Ala Ala Asn Ala Gly Gly Val Ala
 370 375 380
 Val Ser Gly Leu Glu Met Ala Gln Asn Ser Ala Arg Leu Ser Trp Thr
 385 390 395 400
 Ser Glu Glu Val Asp Ala Arg Leu Lys Asp Ile Met Arg Asp Cys Phe
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 Lys Asn Gly Leu Glu Thr Ala Gln Glu Tyr Ala Thr Pro Ala Glu Gly
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